

CD106PCT.ST25
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Plants having increased yield and method for making the same

<130> CD-106-PCT

<150> US 60/532,287

<151> 2003-12-22

<160> 5

<170> PatentIn version 3.3

<210> 1

<211> 1311

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<223> A variant of the coding sequence of the sequence deposited under accession number NM_121168 contains a G instead of C on position 851 and a T instead of C on position 1295

<400> 1

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gtatcaatac ctccaacaaa accttctttt aaacagcaaa agagacgtgc agtacttaag	180
gatgtgagta atacctctgc agatattatt tattcagaac ttcgaaaggg aggcaacatc	240
aaggcaaaca gaaaatgtct aaaagagcct aaaaaagcag caaaggaagg tgctaacagt	300
gccatggata ttctggtaga tatgcataca gaaaaatcaa aattagcaga agatttgtcc	360
aagatcagga tggctgaagc ccaagatgtc tctctttcaa acttttaaaga tgaagaaatt	420
actgagcaac aagaagatgg atcaggtgtc atggagttac ttcaagttgt agatattgat	480
tccaacgtcg aagatccaca gtgttgacgc ttgtatgctg ctgatatata tgacaacata	540
catgtttgag agcttcaaca acgacccttg gctaattata tggagcttgt gcagcgagat	600
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agttacattg aaaggcaaag actccagctc cttggtgtct cttgcatgct tatagcttca	780
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tacacaagac cagaagtgtc gagcatggag attcaaattc taaattttgt gcactttaga	900
ttatcggttc ctaccaccaa aacatttctg aggcggttca ttaaagcagc tcaagcttcg	960
tacaaggtgc ctttcattga actggagtat ttagcaaact atctcgccga attgacactg	1020
gtggaatata gtttcctaag gttcctgcca tcactaattg ctgcttcagc tgttttccta	1080

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gcccgatgga cactcgacca aactgaccat ccttgggaacc ctactctgca acactacacc 1140
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 accagtggct gtactctcgc tgccacccgt gagaaataca accaaccaaa gtttaagagc 1260
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<210> 2
 <211> 436
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> MISC_FEATURE
 <223> A variant of the sequence deposited under accession number
 NP_568248 contains an arginine instead of a proline on position
 284 and a phenylalanine instead of a serine on position 432

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Ser Thr Ser Asp Val Gln Glu Ser Phe Val Arg Ile Thr Arg Ser Arg
20 25 30

Ala Lys Lys Ala Met Gly Arg Gly Val Ser Ile Pro Pro Thr Lys Pro
35 40 45

Ser Phe Lys Gln Gln Lys Arg Arg Ala Val Leu Lys Asp Val Ser Asn
50 55 60

Thr Ser Ala Asp Ile Ile Tyr Ser Glu Leu Arg Lys Gly Gly Asn Ile
65 70 75 80

Lys Ala Asn Arg Lys Cys Leu Lys Glu Pro Lys Lys Ala Ala Lys Glu
85 90 95

Gly Ala Asn Ser Ala Met Asp Ile Leu Val Asp Met His Thr Glu Lys
100 105 110

Ser Lys Leu Ala Glu Asp Leu Ser Lys Ile Arg Met Ala Glu Ala Gln
115 120 125

Asp Val Ser Leu Ser Asn Phe Lys Asp Glu Glu Ile Thr Glu Gln Gln
130 135 140

Glu Asp Gly Ser Gly Val Met Glu Leu Leu Gln Val Val Asp Ile Asp
145 150 155 160

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Ser Asn Val Glu Asp Pro Gln Cys Cys Ser Leu Tyr Ala Ala Asp Ile
 165 170 175
 Tyr Asp Asn Ile His Val Ala Glu Leu Gln Gln Arg Pro Leu Ala Asn
 180 185 190
 Tyr Met Glu Leu Val Gln Arg Asp Ile Asp Pro Asp Met Arg Lys Ile
 195 200 205
 Leu Ile Asp Trp Leu Val Glu Val Ser Asp Asp Tyr Lys Leu Val Pro
 210 215 220
 Asp Thr Leu Tyr Leu Thr Val Asn Leu Ile Asp Arg Phe Leu Ser Asn
 225 230 235 240
 Ser Tyr Ile Glu Arg Gln Arg Leu Gln Leu Leu Gly Val Ser Cys Met
 245 250 255
 Leu Ile Ala Ser Lys Tyr Glu Glu Leu Ser Ala Pro Gly Val Glu Glu
 260 265 270
 Phe Cys Phe Ile Thr Ala Asn Thr Tyr Thr Arg Pro Glu Val Leu Ser
 275 280 285
 Met Glu Ile Gln Ile Leu Asn Phe Val His Phe Arg Leu Ser Val Pro
 290 295 300
 Thr Thr Lys Thr Phe Leu Arg Arg Phe Ile Lys Ala Ala Gln Ala Ser
 305 310 315 320
 Tyr Lys Val Pro Phe Ile Glu Leu Glu Tyr Leu Ala Asn Tyr Leu Ala
 325 330 335
 Glu Leu Thr Leu Val Glu Tyr Ser Phe Leu Arg Phe Leu Pro Ser Leu
 340 345 350
 Ile Ala Ala Ser Ala Val Phe Leu Ala Arg Trp Thr Leu Asp Gln Thr
 355 360 365
 Asp His Pro Trp Asn Pro Thr Leu Gln His Tyr Thr Arg Tyr Glu Val
 370 375 380
 Ala Glu Leu Lys Asn Thr Val Leu Ala Met Glu Asp Leu Gln Leu Asn
 385 390 395 400
 Thr Ser Gly Cys Thr Leu Ala Ala Thr Arg Glu Lys Tyr Asn Gln Pro
 405 410 415

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Lys Phe Lys Ser Val Ala Lys Leu Thr Ser Pro Lys Arg Val Thr Ser
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Leu Phe Ser Arg
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<212> DNA
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ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt 240
attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt 300
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat 360
ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgctaccc 420
atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag 480
gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt 540
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600
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<212> DNA
<213> Artificial sequence

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<223> primer PRM582

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<211> 52
<212> DNA
<213> Artificial sequence

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<223> primer PRM583

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